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-1-

SEQUENCE LISTING

<110> Tanzi, Rudolph
Wasco, Wilma

<120> Genetic Alterations Related To Familial Alzheimer's Disease

<130> 0609.4180002

<140> US 09/785,474

<141> 2001-02-20

<150> US 08/706,344

<151> 1996-08-30

<150> US 60/003,054

<151> 1995-08-31

<160> 32

<170> PatentIn version 3.1

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<222> (249)..(1649)

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ctgggagcct gcaagtgaaca acagcctttg cggctccttag acagcttggc ctggaggaga 180

acacatgaaa gaaagaacct caagaggcct tgttttctgt gaaacagtat ttctatacag 240

ttgctcca atg aca gag tta cct gca ccg ttg tcc tac ttc cag aat gca 290

Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala
1 5 10

cag atg tct gag gac aac cac ctg agc aat act gta cgt agc cag aat 338

Gln Met Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn
15 20 25 30

gac aat aga gaa cgg cag gag cac aac gac aga cgg agc ctt ggc cac 386

Asp Asn Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His



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ccg gaa gct caa agg aga gta tcc aaa aat tcc aag cat aat gca gaa Pro Glu Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu 305 310 315	1202
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ggg ttc agt gag gaa tgg gaa gcc cag agg gac agt cat cta ggg cct Gly Phe Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro 335 340 345 350	1298
cat cgc tct aca cct gag tca cga gct gct gtc cag gaa ctt tcc agc His Arg Ser Thr Pro Glu Ser Arg Ala Val Gln Glu Leu Ser Ser 355 360 365	1346
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cat caa ttt tat atc tagcatat tt gcggttagaa tcccatggat gtttcttctt His Gln Phe Tyr Ile 465	1689
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35 40 45
Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu
50 55 60
Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
65 70 75 80
His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
85 90 95
Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
100 105 110
Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
115 120 125
Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
130 135 140
Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
145 150 155 160
Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe
165 170 175

Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
 180 185 190
 Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val
 195 200 205
 Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
 210 215 220
 Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
 225 230 235 240
 Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
 245 250 255
 Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val
 260 265 270
 Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
 275 280 285
 Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
 290 295 300
 Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu Ser Thr
 305 310 315 320
 Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe
 325 330 335
 Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
 340 345 350
 Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
 355 360 365
 Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
 370 375 380
 Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
 385 390 395 400
 Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
 405 410 415
 Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
 420 425 430
 Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
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 Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala
 1 5 10
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 Gln Met Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn
 15 20 25 30
 gac aat aga gaa cgg cag gag cac aac gac aga cgg agc ctt ggc cac 386
 Asp Asn Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His
 35 40 45
 cct gag cca tta tct aat gga cga ccc cag ggt aac tcc cgg cag gtg 434
 Pro Glu Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val
 50 55 60
 gtg gag caa gat gag gaa gaa gat gag gag ctg aca ttg aaa tat ggc 482
 Val Glu Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly
 65 70 75
 gcc aag cat gtg atc atg ctc ttt gtc cct gtg act ctc tgc atg gtg 530
 Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val
 80 85 90
 gtg gtc gtg gct acc att aag tca gtc agc ttt tat acc cgg aag gat 578
 Val Val Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp
 95 100 105 110
 ggg cag cta atc tat acc cca ttc aca gaa gat acc gag act gtg ggc 626
 Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly
 115 120 125
 cag aga gcc ctg cac tca att ctg aat gct gcc atc atg atc agt gtc 674
 Gln Arg Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val
 130 135 140
 att gtt gtc atg act atc ctc ctg gtg gtt ctg tat aaa tac agg tgc 722
 Ile Val Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys
 145 150 155
 tat aag gtc atc cat gcc tgg ctt att ata tca tct cta ttg ttg ctg 770
 Tyr Lys Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu
 160 165 170
 ttc ttt ttt tca ttc att tac ttg ggg gaa gtg ttt aaa acc tat aac 818
 Phe Phe Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn

gca ttg cca gct ctt cca atc tcc atc acc ttt ggg ctt gtt ttc tac 1586
Ala Leu Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr
435 440 445

ttt gcc aca gat tat ctt gta cag cct ttt atg gac caa tta gca ttc 1634
Phe Ala Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe
450 455 460

cat caa ttt tat atc tagcatattt gcggttagaa tcccatggat gtttcttctt 1689
His Gln Phe Tyr Ile
465

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attggacttt ggaaggaggt gcctatagaa aacgattttg aacatacttc atcgcaagtgg 1869

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ggccccgaag ttgctgtgcc ccacgcagcag cttgacgcgt ggtcacagga cgatttcact 1989

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<213> Homo sapiens

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His	Val	Ile	Met	Leu	Phe	Val	Pro	Val	Thr	Leu	Cys	Met	Val	Val	Val
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Val	Ala	Thr	Ile	Lys	Ser	Val	Ser	Phe	Tyr	Thr	Arg	Lys	Asp	Gly	Gln
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Leu	Ile	Tyr	Thr	Pro	Phe	Thr	Glu	Asp	Thr	Glu	Thr	Val	Gly	Gln	Arg
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Val	Met	Thr	Ile	Leu	Leu	Val	Val	Leu	Tyr	Lys	Tyr	Arg	Cys	Tyr	Lys
145				150					155						160
Val	Ile	His	Ala	Trp	Leu	Ile	Ile	Ser	Ser	Leu	Leu	Leu	Leu	Phe	Phe
				165					170					175	
Phe	Ser	Phe	Ile	Tyr	Leu	Gly	Glu	Val	Phe	Lys	Thr	Tyr	Asn	Val	Ala
			180					185					190		
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Gly	Met	Ile	Ser	Ile	His	Trp	Lys	Gly	Pro	Leu	Arg	Leu	Gln	Gln	Ala
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225					230					235					240
Leu	Pro	Glu	Trp	Thr	Ala	Trp	Leu	Ile	Leu	Ala	Val	Ile	Ser	Val	Tyr
				245					250					255	
Asp	Leu	Val	Ala	Val	Leu	Arg	Leu	Lys	Gly	Pro	Leu	His	Met	Leu	Val
			260					265					270		
Glu	Thr	Ala	Gln	Glu	Arg	Asn	Glu	Thr	Leu	Phe	Pro	Ala	Leu	Ile	Tyr
		275					280					285			
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Glu	Arg	Glu	Ser	Gln	Asp	Thr	Val	Ala	Glu	Asn	Asp	Asp	Gly	Gly	Phe
				325					330					335	
Ser	Glu	Glu	Trp	Glu	Ala	Gln	Arg	Asp	Ser	His	Leu	Gly	Pro	His	Arg
			340					345					350		
Ser	Thr	Pro	Glu	Ser	Arg	Ala	Ala	Val	Gln	Glu	Leu	Ser	Ser	Ser	Ile
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Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
370 375 380

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385 390 395 400

Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
405 410 415

Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
420 425 430

Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
435 440 445

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450 455 460

Phe Tyr Ile
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 Phe Leu Leu Gln Thr His Pro Phe
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<400> 21
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Cys Asp Cys His Phe Phe Pro Arg Pro Val
20 25

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Phe Trp Lys Gln Tyr Ser Tyr Phe Ser Ser Ile Leu Tyr His Val Glu
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Val Lys Phe Gly Phe Ser Thr Lys Phe
35 40

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acacatgaaa gaaagaacct caagaggctt tgttttctgt gaaacagtat ttctatacag 240
ttgctcca atg aca gag tta cct gca ccg ttg tcc tac ttc cag aat gca 290
Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala
1 5 10
cag atg tct gag gac aac cac ctg agc aat act gta cgt agc cag aat 338
Gln Met Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn
15 20 25 30
gac aat aga gaa cgg cag gag cac aac gac aga cgg agc ctt ggc cac 386
Asp Asn Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His
35 40 45
cct gag cca tta tct aat gga cga ccc cag ggt aac tcc cgg cag gtg 434
Pro Glu Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val
50 55 60
gtg gag caa gat gag gaa gaa gat gag gag ctg aca ttg aaa tat ggc 482
Val Glu Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly
65 70 75
gcc aag cat gtg atc atg ctc ttt gtc cct gtg act ctc tgc atg gtg 530
Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val
80 85 90
gtg gtc gtg gct acc att aag tca gtc agc ttt tat acc cgg aag gat 578
Val Val Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp

95		100		105		110	
ggg cag cta atc tat acc cca ttc aca gaa gat acc gag act gtg ggc	626						
Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly							
		115		120		125	
cag aga gcc ctg cac tca att ctg aat gct gcc atc atg atc agt gtc	674						
Gln Arg Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val							
		130		135		140	
att gtt gtc atg act atc ctc ctg gtg gtt ctg tat aaa tac agg tgc	722						
Ile Val Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys							
		145		150		155	
tat aag gtc atc cat gcc tgg ctt att ata tca tct cta ttg ttg ctg	770						
Tyr Lys Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu							
		160		165		170	
ttc ttt ttt tca ttc att tac ttg ggg gaa gtg ttt aaa acc tat aac	818						
Phe Phe Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn							
		175		180		185	190
gtt gct gtg gac tac att act gtt gca ctc ctg atc tgg aat ttt ggt	866						
Val Ala Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly							
		195		200		205	
gtg gtg gga atg att tcc att cac tgg aaa ggt cca ctt cga ctc cag	914						
Val Val Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln							
		210		215		220	
cag gca tat ctc att atg att agt gcc ctc atg gcc ctg gtg ttt atc	962						
Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile							
		225		230		235	
aag tac ctc cct gaa tgg act gcg tgg ctc atc ttg gct gtg att tca	1010						
Lys Tyr Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser							
		240		245		250	
gta tat gat tta gtg gct gtt ttg cgt ccg aaa ggt cca ctt cgt atg	1058						
Val Tyr Asp Leu Val Ala Val Leu Arg Pro Lys Gly Pro Leu Arg Met							
		255		260		265	270
ctg gtt gaa aca gct cag gag aga aat gaa acg ctt ttt cca gct ctc	1106						
Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu							
		275		280		285	
att tac tcc tca aca atg gtg tgg ttg gtg aat atg gca gaa gga gac	1154						
Ile Tyr Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp							
		290		295		300	
ccg gaa gct caa agg aga gta tcc aaa aat tcc aag cat aat gca gaa	1202						
Pro Glu Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu							
		305		310		315	
agc aca gaa agg gag tca caa gac act gtt gca gag aat gat gat ggc	1250						
Ser Thr Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly							
		320		325		330	
ggg ttc agt gag gaa tgg gaa gcc cag agg gac agt cat cta ggg cct	1298						
Gly Phe Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro							
		335		340		345	350

cat cgc tct aca cct gag tca cga gct gct gtc cag gaa ctt tcc agc	1346
His Arg Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser	
355 360 365	
agt atc ctc gct ggt gaa gac cca gag gaa agg gga gta aaa ctt gga	1394
Ser Ile Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly	
370 375 380	
ttg gga gat ttc att ttc tac agt gtt ctg gtt ggt aaa gcc tca gca	1442
Leu Gly Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala	
385 390 395	
aca gcc agt gga gac tgg aac aca acc ata gcc tgt ttc gta gcc ata	1490
Thr Ala Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile	
400 405 410	
tta att ggt ttg tgc ctt aca tta tta ctc ctt gcc att ttc aag aaa	1538
Leu Ile Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys	
415 420 425 430	
gca ttg cca gct ctt cca atc tcc atc acc ttt ggg ctt gtt ttc tac	1586
Ala Leu Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr	
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ttt gcc aca gat tat ctt gta cag cct ttt atg gac caa tta gca ttc	1634
Phe Ala Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe	
450 455 460	
cat caa ttt tat atc tagcatatct gcggttagaa tcccatggat gtttcttctt	1689
His Gln Phe Tyr Ile	
465	
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aatggagagg tgggcagggg ttccagcttc ctttgattt tttgctgcag actcatcctt	2229
tttaaagtga acttggtttt cctctctttt gagtcaagtc aaatatgtag attgcctttg	2289
gcaattcttc ttctcaagca ctgacactca ttaccgtctg tgattgccat ttcttcccaa	2349
ggccagtctg aacctgaggt tgctttatcc taaaagtttt aacctcaggt tccaaattca	2409
gtaaattttg gaaacagtac agctatttct catcaattct ctatcatggt gaagtcaaat	2469
ttggattttt caccaaaattc tgaatttgta gacatacttg tacgctcact tgccccaga	2529
tgctctctct gtctcattc ttctctccca cacaagcagt ctttttctac agccagtaag	2589

gcagctctgt crtggtagca gatgggtccca ttattctagg gtcttactct ttgtatgatg 2649
 aaaagaatgt gttatgaatc ggtgctgtca gccctgctgt cagaccttct tccacagcaa 2709
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 <211> 467
 <212> PRT
 <213> Homo sapiens

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 Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu
 35 40 45
 Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu
 50 55 60
 Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
 65 70 75 80
 His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
 85 90 95
 Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
 100 105 110
 Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
 115 120 125
 Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
 130 135 140
 Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
 145 150 155 160
 Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe
 165 170 175
 Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
 180 185 190
 Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val
 195 200 205
 Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
 210 215 220
 Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
 225 230 235 240
 Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
 245 250 255

Asp Leu Val Ala Val Leu Arg Pro Lys Gly Pro Leu Arg Met Leu Val
260 265 270

Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
275 280 285

Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
290 295 300

Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu Ser Thr
305 310 315 320

Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe
325 330 335

Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
340 345 350

Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
355 360 365

Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
370 375 380

Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
385 390 395 400

Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
405 410 415

Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
420 425 430

Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
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450 455 460

Phe Tyr Ile
465

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<211> 2765
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<220>
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acacatgaaa gaaagaacct caagaggctt tgttttctgt gaaacagtat ttctatacag	240
ttgctcca atg aca gag tta cct gca ccg ttg tcc tac ttc cag aat gca	290
Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala	
1 5 10	
cag atg tct gag gac aac cac ctg agc aat act gta cgt agc cag aat	338
Gln Met Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn	
15 20 25 30	
gac aat aga gaa cgg cag gag cac aac gac aga cgg agc ctt ggc cac	386
Asp Asn Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His	
35 40 45	
cct gag cca tta tct aat gga cga ccc cag ggt aac tcc cgg cag gtg	434
Pro Glu Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val	
50 55 60	
gtg gag caa gat gag gaa gaa gat gag gag ctg aca ttg aaa tat ggc	482
Val Glu Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly	
65 70 75	
gcc aag cat gtg atc atg ctc ttt gtc cct gtg act ctc tgc atg gtg	530
Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val	
80 85 90	
gtg gtc gtg gct acc att aag tca gtc agc ttt tat acc cgg aag gat	578
Val Val Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp	
95 100 105 110	
ggg cag cta atc tat acc cca ttc aca gaa gat acc gag act gtg ggc	626
Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly	
115 120 125	
cag aga gcc ctg cac tca att ctg aat gct gcc atc atg atc agt gtc	674
Gln Arg Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val	
130 135 140	
att gtt gtc atg act atc ctc ctg gtg gtt ctg tat aaa tac agg tgc	722
Ile Val Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys	
145 150 155	
tat aag gtc atc cat gcc tgg ctt att ata tca tct cta ttg ttg ctg	770
Tyr Lys Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu	
160 165 170	
ttc ttt ttt tca ttc att tac ttg ggg gaa gtg ttt aaa acc tat aac	818
Phe Phe Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn	
175 180 185 190	
gtt gct gtg gac tac att act gtt gca ctc ctg atc tgg aat ttt ggt	866
Val Ala Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly	
195 200 205	
gtg gtg gga atg att tcc att cac tgg aaa ggt cca ctt cga ctc cag	914
Val Val Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln	
210 215 220	
cag gca tat ctc att atg att agt gcc ctc atg gcc ctg gtg ttt atc	962
Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile	
225 230 235	

aag tac ctc cct gaa tgg act gcg tgg ctc atc ttg gct gtg att tca	1010
Lys Tyr Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser	
240 245 250	
gta tat gat tta gtg gct gtt ttg tgt ctg aaa ggt cca ctt cgt atg	1058
Val Tyr Asp Leu Val Ala Val Leu Cys Leu Lys Gly Pro Leu Arg Met	
255 260 265 270	
ctg gtt gaa aca gct cag gag aga aat gaa acg ctt ttt cca gct ctc	1106
Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu	
275 280 285	
att tac tcc tca aca atg gtg tgg ttg gtg aat atg gca gaa gga gac	1154
Ile Tyr Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp	
290 295 300	
ccg gaa gct caa agg aga gta tcc aaa aat tcc aag cat aat gca gaa	1202
Pro Glu Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu	
305 310 315	
agc aca gaa agg gag tca caa gac act gtt gca gag aat gat gat ggc	1250
Ser Thr Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly	
320 325 330	
ggg ttc agt gag gaa tgg gaa gcc cag agg gac agt cat cta ggg cct	1298
Gly Phe Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro	
335 340 345 350	
cat cgc tct aca cct gag tca cga gct gct gtc cag gaa ctt tcc agc	1346
His Arg Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser	
355 360 365	
agt atc ctc gct ggt gaa gac cca gag gaa agg gga gta aaa ctt gga	1394
Ser Ile Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly	
370 375 380	
ttg gga gat ttc att ttc tac agt gtt ctg gtt ggt aaa gcc tca gca	1442
Leu Gly Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala	
385 390 395	
aca gcc agt gga gac tgg aac aca acc ata gcc tgt ttc gta gcc ata	1490
Thr Ala Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile	
400 405 410	
tta att ggt ttg tgc ctt aca tta tta ctc ctt gcc att ttc aag aaa	1538
Leu Ile Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys	
415 420 425 430	
gca ttg cca gct ctt cca atc tcc atc acc ttt ggg ctt gtt ttc tac	1586
Ala Leu Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr	
435 440 445	
ttt gcc aca gat tat ctt gta cag cct ttt atg gac caa tta gca ttc	1634
Phe Ala Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe	
450 455 460	
cat caa ttt tat atc tagcatatctt gcggttagaa tcccatggat gtttcttctt	1689
His Gln Phe Tyr Ile	
465	
tgactataac caaatctggg gaggacaaag gtgattttcc tgtgtccaca tctaacaaag	1749

tcaagattcc cggtggact tttgcagctt cttccaagt cttcctgacc accttgcaact 1809
attggacttt ggaaggaggt gcctatagaa aacgattttg aacatacttc atcgcagtgg 1869
actgtgtccc tcggtgcaga aactaccaga tttgagggac gaggtcaagg agatatgata 1929
ggccccgaag ttgctgtgcc ccatcagcag cttgacgcgt ggtcacagga cgatttcact 1989
gacactgcga actctcagga ctaccgggta ccaagaggtt aggtgaagtg gtttaaacca 2049
aacggaactc ttcattctaa actacacgtt gaaaatcaac ccaataattc tgtattaact 2109
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gtaaattttg gaaacagtac agctatttct catcaattct ctatcatgtt gaagtcaaatt 2469
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aaaagaatgt gttatgaatc ggtgctgtca gccctgctgt cagaccttct tccacagcaa 2709
atgagatgta tgcccaaagc ggtagaatta aagaagagta aaatggctgt tgaagc 2765

<210> 30
<211> 467
<212> PRT
<213> Homo sapiens

<400> 30
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Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn
20 25 30
Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu
35 40 45
Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu
50 55 60
Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
65 70 75 80
His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
85 90 95
Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
100 105 110

Leu	Ile	Tyr	Thr	Pro	Phe	Thr	Glu	Asp	Thr	Glu	Thr	Val	Gly	Gln	Arg	115	120	125
Ala	Leu	His	Ser	Ile	Leu	Asn	Ala	Ala	Ile	Met	Ile	Ser	Val	Ile	Val	130	135	140
Val	Met	Thr	Ile	Leu	Leu	Val	Val	Leu	Tyr	Lys	Tyr	Arg	Cys	Tyr	Lys	145	150	155
Val	Ile	His	Ala	Trp	Leu	Ile	Ile	Ser	Ser	Leu	Leu	Leu	Leu	Phe	Phe	165	170	175
Phe	Ser	Phe	Ile	Tyr	Leu	Gly	Glu	Val	Phe	Lys	Thr	Tyr	Asn	Val	Ala	180	185	190
Val	Asp	Tyr	Ile	Thr	Val	Ala	Leu	Leu	Ile	Trp	Asn	Phe	Gly	Val	Val	195	200	205
Gly	Met	Ile	Ser	Ile	His	Trp	Lys	Gly	Pro	Leu	Arg	Leu	Gln	Gln	Ala	210	215	220
Tyr	Leu	Ile	Met	Ile	Ser	Ala	Leu	Met	Ala	Leu	Val	Phe	Ile	Lys	Tyr	225	230	235
Leu	Pro	Glu	Trp	Thr	Ala	Trp	Leu	Ile	Leu	Ala	Val	Ile	Ser	Val	Tyr	245	250	255
Asp	Leu	Val	Ala	Val	Leu	Cys	Leu	Lys	Gly	Pro	Leu	Arg	Met	Leu	Val	260	265	270
Glu	Thr	Ala	Gln	Glu	Arg	Asn	Glu	Thr	Leu	Phe	Pro	Ala	Leu	Ile	Tyr	275	280	285
Ser	Ser	Thr	Met	Val	Trp	Leu	Val	Asn	Met	Ala	Glu	Gly	Asp	Pro	Glu	290	295	300
Ala	Gln	Arg	Arg	Val	Ser	Lys	Asn	Ser	Lys	His	Asn	Ala	Glu	Ser	Thr	305	310	315
Glu	Arg	Glu	Ser	Gln	Asp	Thr	Val	Ala	Glu	Asn	Asp	Asp	Gly	Gly	Phe	325	330	335
Ser	Glu	Glu	Trp	Glu	Ala	Gln	Arg	Asp	Ser	His	Leu	Gly	Pro	His	Arg	340	345	350
Ser	Thr	Pro	Glu	Ser	Arg	Ala	Ala	Val	Gln	Glu	Leu	Ser	Ser	Ser	Ile	355	360	365
Leu	Ala	Gly	Glu	Asp	Pro	Glu	Glu	Arg	Gly	Val	Lys	Leu	Gly	Leu	Gly	370	375	380
Asp	Phe	Ile	Phe	Tyr	Ser	Val	Leu	Val	Gly	Lys	Ala	Ser	Ala	Thr	Ala	385	390	395
Ser	Gly	Asp	Trp	Asn	Thr	Thr	Ile	Ala	Cys	Phe	Val	Ala	Ile	Leu	Ile	405	410	415
Gly	Leu	Cys	Leu	Thr	Leu	Leu	Leu	Leu	Ala	Ile	Phe	Lys	Lys	Ala	Leu	420	425	430
Pro	Ala	Leu	Pro	Ile	Ser	Ile	Thr	Phe	Gly	Leu	Val	Phe	Tyr	Phe	Ala	435	440	445

Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
450 455 460

Phe Tyr Ile
465

<210> 31
<211> 2765
<212> DNA
<213> Homo sapiens

<220>
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<222> (249) .. (1649)
<223>

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ctgggagcct gcaagtgaca acagcctttg cggtccttag acagcttggc ctggaggaga 180
acacatgaaa gaaagaacct caagaggctt tgttttctgt gaaacagtat ttctatacag 240
ttgctcca atg aca gag tta cct gca ccg ttg tcc tac ttc cag aat gca 290
Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala
1 5 10
cag atg tct gag gac aac cac ctg agc aat act gta cgt agc cag aat 338
Gln Met Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn
15 20 25 30
gac aat aga gaa cgg cag gag cac aac gac aga cgg agc ctt ggc cac 386
Asp Asn Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His
35 40 45
cct gag cca tta tct aat gga cga ccc cag ggt aac tcc cgg cag gtg 434
Pro Glu Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val
50 55 60
gtg gag caa gat gag gaa gaa gat gag gag ctg aca ttg aaa tat ggc 482
Val Glu Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly
65 70 75
gcc aag cat gtg atc atg ctc ttt gtc cct gtg act ctc tgc atg gtg 530
Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val
80 85 90
gtg gtc gtg gct acc att aag tca gtc agc ttt tat acc cgg aag gat 578
Val Val Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp
95 100 105 110
ggg cag cta atc tat acc cca ttc aca gaa gat acc gag act gtg ggc 626
Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly
115 120 125
cag aga gcc ctg cac tca att ctg aat gct gcc atc atg atc agt gtc 674
Gln Arg Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val

	130		135		140	
att gtt gtc atg act atc ctc ctg gtt gtt ctg tat aaa tac agg tgc						722
Ile Val Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys						
	145		150		155	
tat aag gtc atc cat gcc tgg ctt att ata tca tct cta ttg ttg ctg						770
Tyr Lys Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu						
	160		165		170	
ttc ttt ttt tca ttc att tac ttg ggg gaa gtg ttt aaa acc tat aac						818
Phe Phe Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn						
	175		180		185	190
gtt gct gtg gac tac att act gtt gca ctc ctg atc tgg aat ttt ggt						866
Val Ala Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly						
	195		200		205	
gtg gtg gga atg att tcc att cac tgg aaa ggt cca ctt cga ctc cag						914
Val Val Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln						
	210		215		220	
cag gca tat ctc att atg att agt gcc ctc atg gcc ctg gtg ttt atc						962
Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile						
	225		230		235	
aag tac ctc cct gaa tgg act gcg tgg ctc atc ttg gct gtg att tca						1010
Lys Tyr Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser						
	240		245		250	
gta tat gat tta gtg gct gtt ttg tgt ccg aaa ggt cca ctt cat atg						1058
Val Tyr Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu His Met						
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ctg gtt gaa aca gct cag gag aga aat gaa acg ctt ttt cca gct ctc						1106
Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu						
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att tac tcc tca aca atg gtg tgg ttg gtg aat atg gca gaa gga gac						1154
Ile Tyr Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp						
	290		295		300	
ccg gaa gct caa agg aga gta tcc aaa aat tcc aag cat aat gca gaa						1202
Pro Glu Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu						
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agc aca gaa agg gag tca caa gac act gtt gca gag aat gat gat ggc						1250
Ser Thr Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly						
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Gly Phe Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro						
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cat cgc tct aca cct gag tca cga gct gct gtc cag gaa ctt tcc agc						1346
His Arg Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser						
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agt atc ctc gct ggt gaa gac cca gag gaa agg gga gta aaa ctt gga						1394
Ser Ile Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly						
	370		375		380	

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Leu Gly Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala	
385 390 395	
aca gcc agt gga gac tgg aac aca acc ata gcc tgt ttc gta gcc ata	1490
Thr Ala Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile	
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tta att ggt ttg tgc ctt aca tta tta ctc ctt gcc att ttc aag aaa	1538
Leu Ile Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys	
415 420 425 430	
gca ttg cca gct ctt cca atc tcc atc acc ttt ggg ctt gtt ttc tac	1586
Ala Leu Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr	
435 440 445	
ttt gcc aca gat tat ctt gta cag cct ttt atg gac caa tta gca ttc	1634
Phe Ala Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe	
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His Gln Phe Tyr Ile	
465	
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 <212> PRT
 <213> Homo sapiens

<400> 32

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Arg	Glu	Arg	Gln	Glu	His	Asn	Asp	Arg	Arg	Ser	Leu	Gly	His	Pro	Glu
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Pro	Leu	Ser	Asn	Gly	Arg	Pro	Gln	Gly	Asn	Ser	Arg	Gln	Val	Val	Glu
	50					55					60				
Gln	Asp	Glu	Glu	Glu	Asp	Glu	Glu	Leu	Thr	Leu	Lys	Tyr	Gly	Ala	Lys
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His	Val	Ile	Met	Leu	Phe	Val	Pro	Val	Thr	Leu	Cys	Met	Val	Val	Val
				85					90					95	
Val	Ala	Thr	Ile	Lys	Ser	Val	Ser	Phe	Tyr	Thr	Arg	Lys	Asp	Gly	Gln
			100					105					110		
Leu	Ile	Tyr	Thr	Pro	Phe	Thr	Glu	Asp	Thr	Glu	Thr	Val	Gly	Gln	Arg
		115					120					125			
Ala	Leu	His	Ser	Ile	Leu	Asn	Ala	Ala	Ile	Met	Ile	Ser	Val	Ile	Val
	130					135					140				
Val	Met	Thr	Ile	Leu	Leu	Val	Val	Leu	Tyr	Lys	Tyr	Arg	Cys	Tyr	Lys
145					150					155					160
Val	Ile	His	Ala	Trp	Leu	Ile	Ile	Ser	Ser	Leu	Leu	Leu	Leu	Phe	Phe
				165					170					175	
Phe	Ser	Phe	Ile	Tyr	Leu	Gly	Glu	Val	Phe	Lys	Thr	Tyr	Asn	Val	Ala
			180					185					190		
Val	Asp	Tyr	Ile	Thr	Val	Ala	Leu	Leu	Ile	Trp	Asn	Phe	Gly	Val	Val
		195					200					205			
Gly	Met	Ile	Ser	Ile	His	Trp	Lys	Gly	Pro	Leu	Arg	Leu	Gln	Gln	Ala
	210					215					220				
Tyr	Leu	Ile	Met	Ile	Ser	Ala	Leu	Met	Ala	Leu	Val	Phe	Ile	Lys	Tyr
225					230					235					240
Leu	Pro	Glu	Trp	Thr	Ala	Trp	Leu	Ile	Leu	Ala	Val	Ile	Ser	Val	Tyr
				245					250					255	
Asp	Leu	Val	Ala	Val	Leu	Cys	Pro	Lys	Gly	Pro	Leu	His	Met	Leu	Val
			260					265					270		
Glu	Thr	Ala	Gln	Glu	Arg	Asn	Glu	Thr	Leu	Phe	Pro	Ala	Leu	Ile	Tyr
		275					280					285			
Ser	Ser	Thr	Met	Val	Trp	Leu	Val	Asn	Met	Ala	Glu	Gly	Asp	Pro	Glu
	290					295					300				

Ala	Gln	Arg	Arg	Val	Ser	Lys	Asn	Ser	Lys	His	Asn	Ala	Glu	Ser	Thr	305	310	315	320
Glu	Arg	Glu	Ser	Gln	Asp	Thr	Val	Ala	Glu	Asn	Asp	Asp	Gly	Gly	Phe	325	330	335	
Ser	Glu	Glu	Trp	Glu	Ala	Gln	Arg	Asp	Ser	His	Leu	Gly	Pro	His	Arg	340	345	350	
Ser	Thr	Pro	Glu	Ser	Arg	Ala	Ala	Val	Gln	Glu	Leu	Ser	Ser	Ser	Ile	355	360	365	
Leu	Ala	Gly	Glu	Asp	Pro	Glu	Glu	Arg	Gly	Val	Lys	Leu	Gly	Leu	Gly	370	375	380	
Asp	Phe	Ile	Phe	Tyr	Ser	Val	Leu	Val	Gly	Lys	Ala	Ser	Ala	Thr	Ala	385	390	395	400
Ser	Gly	Asp	Trp	Asn	Thr	Thr	Ile	Ala	Cys	Phe	Val	Ala	Ile	Leu	Ile	405	410	415	
Gly	Leu	Cys	Leu	Thr	Leu	Leu	Leu	Leu	Ala	Ile	Phe	Lys	Lys	Ala	Leu	420	425	430	
Pro	Ala	Leu	Pro	Ile	Ser	Ile	Thr	Phe	Gly	Leu	Val	Phe	Tyr	Phe	Ala	435	440	445	
Thr	Asp	Tyr	Leu	Val	Gln	Pro	Phe	Met	Asp	Gln	Leu	Ala	Phe	His	Gln	450	455	460	
Phe	Tyr	Ile														465			